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## RAW SEQUENCE LISTING

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Application Serial Number: 1015191465A  
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PCT

## RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/519,465A

TIME: 10:36:49

Input Set : A:\3190-069 Sequence Listing.txt

Output Set: N:\CRF4\01132006\J519465A.raw

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3 <110> APPLICANT: DOI, Hirofumi
4     HOSOGI, Shinya
5     WADA, Naoya
7 <120> TITLE OF INVENTION: MKK7 Activation Inhibitor
9 <130> FILE REFERENCE: 3190-069
11 <140> CURRENT APPLICATION NUMBER: 10/519,465A
12 <141> CURRENT FILING DATE: 2004-12-27
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/008179
15 <151> PRIOR FILING DATE: 2003-06-27
17 <150> PRIOR APPLICATION NUMBER: JP P 2002-190909
18 <151> PRIOR FILING DATE: 2002-06-28
20 <150> PRIOR APPLICATION NUMBER: JP P 2002-190910
21 <151> PRIOR FILING DATE: 2002-06-28
23 <160> NUMBER OF SEQ ID NOS: 46
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 7
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: MISC_FEATURE
34 <223> OTHER INFORMATION: Partial sequence of MKK7, which is highly homologous to that
(SEQ
35     ID NO:3) of PAK4
38 <400> SEQUENCE: 1
40 Asp Val Trp Ser Leu Gly Ile
41 1           5
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 6
45 <212> TYPE: PRT
46 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: MISC_FEATURE
50 <223> OTHER INFORMATION: Partial sequence of MKK7, which is highly homologous to that
(SEQ
51     ID NO:4) of PAK4
54 <400> SEQUENCE: 2
58 Pro Pro Ala Arg Pro Arg
59 1           5
62 <210> SEQ ID NO: 3
63 <211> LENGTH: 7
64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapiens
67 <220> FEATURE:

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68 <221> NAME/KEY: MISC\_FEATURE

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69 <223> OTHER INFORMATION: Partial sequence of PAK4, which is highly homologous to that
(SEQ
70      ID NO:1) of MKK7
73 <400> SEQUENCE: 3
75 Asp Ile Trp Ser Leu Gly Ile
76 1      5
79 <210> SEQ ID NO: 4
80 <211> LENGTH: 6
81 <212> TYPE: PRT
82 <213> ORGANISM: Homo sapiens
84 <220> FEATURE:
85 <221> NAME/KEY: MISC_FEATURE
86 <223> OTHER INFORMATION: Partial sequence of PAK4, which is highly homologous to that
(SEQ
87      ID NO:2) of MKK7
90 <400> SEQUENCE: 4
92 Pro Pro Ala Arg Ala Arg
93 1      5
96 <210> SEQ ID NO: 5
97 <211> LENGTH: 6
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <220> FEATURE:
102 <221> NAME/KEY: misc_feature
103 <223> OTHER INFORMATION: Partial sequence of MKK7, which is highly homologous to that
(SEQ
104      ID NO:7) of JIK
107 <400> SEQUENCE: 5
109 Trp Ser Leu Gly Ile Ser
110 1      5
116 <210> SEQ ID NO: 6
117 <211> LENGTH: 6
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <223> OTHER INFORMATION: Partial sequence of MKK7, which is highly homologous to that
(SEQ
124      ID NO:8) of JIK
127 <400> SEQUENCE: 6
129 Leu Glu Ala Lys Leu Lys
130 1      5
133 <210> SEQ ID NO: 7
134 <211> LENGTH: 6
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <220> FEATURE:
139 <221> NAME/KEY: misc_feature
140 <223> OTHER INFORMATION: Partial sequence of JIK, which is highly homologous to that
(SEQ
141      ID NO:5) of MKK7
144 <400> SEQUENCE: 7
146 Trp Ser Leu Gly Ile Thr

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147 1

5



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150 <210> SEQ ID NO: 8
151 <211> LENGTH: 6
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
155 <220> FEATURE:
156 <221> NAME/KEY: misc_feature
157 <223> OTHER INFORMATION: Partial sequence of JIK, which is highly homologous to that
(SEQ
158      ID NO:6) of MKK7
161 <400> SEQUENCE: 8
163 Leu Glu Asn Lys Leu Lys
164 1      5
167 <210> SEQ ID NO: 9
168 <211> LENGTH: 24
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
173 <220> FEATURE:
174 <221> NAME/KEY: MISC_FEATURE
175 <223> OTHER INFORMATION: Partial sequence of MKK7, showing high score in the local
alignment
176      between MKK7 and PAK4
179 <400> SEQUENCE: 9
181 Tyr Asp Ile Arg Ala Asp Val Trp Ser Leu Gly Ile Ser Leu Val Glu
182 1      5      10      15
185 Leu Ala Thr Gly Gln Phe Pro Tyr
186      20
189 <210> SEQ ID NO: 10
190 <211> LENGTH: 24
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
194 <220> FEATURE:
195 <221> NAME/KEY: misc_feature
196 <223> OTHER INFORMATION: Partial sequence of PAK4, showing high score in the local
alignment
197      between MKK7 and PAK4
200 <400> SEQUENCE: 10
202 Tyr Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu
203 1      5      10      15
206 Met Val Asp Gly Glu Pro Pro Tyr
207      20
210 <210> SEQ ID NO: 11
211 <211> LENGTH: 5
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
215 <220> FEATURE:
216 <221> NAME/KEY: misc_feature
217 <223> OTHER INFORMATION: Partial sequence identical in the sequences of MKK7, PAK4
and JIK
220 <400> SEQUENCE: 11
222 Trp Ser Leu Gly Ile
223 1      5
230 <210> SEQ ID NO: 12
231 <211> LENGTH: 32

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232 <212> TYPE: PRT
233 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
236 <221> NAME/KEY: MISC_FEATURE
237 <223> OTHER INFORMATION: Partial sequence of MKK7, showing high score in the local
alignment
238         between MKK7 and PAK4
241 <400> SEQUENCE: 12
243 Leu Glu Asn Leu Gly Glu Met Gly Ser Gly Thr Cys Gly Gln Val Trp
244 1             5             10             15
247 Lys Met Arg Phe Arg Lys Thr Gly His Val Ile Ala Val Lys Gln Met
248         20             25             30
251 <210> SEQ ID NO: 13
252 <211> LENGTH: 32
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <221> NAME/KEY: misc_feature
258 <223> OTHER INFORMATION: Partial sequence of PAK4, showing high score in the local
alignment
259         between MKK7 and PAK4
262 <400> SEQUENCE: 13
264 Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile Val Cys
265 1             5             10             15
268 Ile Ala Thr Val Arg Ser Ser Gly Lys Leu Val Ala Val Lys Lys Met
269         20             25             30
272 <210> SEQ ID NO: 14
273 <211> LENGTH: 14
274 <212> TYPE: PRT
275 <213> ORGANISM: Homo sapiens
277 <220> FEATURE:
278 <221> NAME/KEY: MISC_FEATURE
279 <223> OTHER INFORMATION: Partial sequence of MKK7, showing high score in the local
alignment
280         between MKK7 and PAK4
283 <400> SEQUENCE: 14
287 Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro
288 1             5             10
291 <210> SEQ ID NO: 15
292 <211> LENGTH: 14
293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <223> OTHER INFORMATION: Partial sequence of PAK4, showing high score in the local
alignment
299         between MKK7 and PAK4
302 <400> SEQUENCE: 15
304 Pro Pro Pro Pro Ala Arg Ala Arg Gln Glu Asn Gly Met Pro
305 1             5             10
308 <210> SEQ ID NO: 16
309 <211> LENGTH: 4
310 <212> TYPE: PRT

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311 &lt;213&gt; ORGANISM: Homo sapiens

313 &lt;220&gt; FEATURE:

314 &lt;221&gt; NAME/KEY: misc\_feature

315 &lt;223&gt; OTHER INFORMATION: Partial sequence identical in the sequences of MKK7 and PAK4

318 &lt;400&gt; SEQUENCE: 16

320 Pro Pro Ala Arg

321 1

324 &lt;210&gt; SEQ ID NO: 17

325 &lt;211&gt; LENGTH: 22

326 &lt;212&gt; TYPE: PRT

327 &lt;213&gt; ORGANISM: Homo sapiens

329 &lt;220&gt; FEATURE:

330 &lt;221&gt; NAME/KEY: misc\_feature

331 &lt;223&gt; OTHER INFORMATION: Partial sequence of MKK7, showing high score in the local alignment

332 between MKK7 and PAK4

335 &lt;400&gt; SEQUENCE: 17

337 Leu Thr Lys Asp His Arg Lys Arg Pro Lys Tyr Asn Lys Leu Leu Glu

338 1 5 10 15

341 His Ser Phe Ile Lys Arg

342 20

345 &lt;210&gt; SEQ ID NO: 18

346 &lt;211&gt; LENGTH: 22

347 &lt;212&gt; TYPE: PRT

348 &lt;213&gt; ORGANISM: Homo sapiens

350 &lt;220&gt; FEATURE:

351 &lt;221&gt; NAME/KEY: misc\_feature

352 &lt;223&gt; OTHER INFORMATION: Partial sequence of PAK4, showing high score in the local alignment

353 between MKK7 and PAK4

356 &lt;400&gt; SEQUENCE: 18

358 Leu Val Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys

359 1 5 10 15

361 His Pro Phe Leu Ala Lys

362 20

365 &lt;210&gt; SEQ ID NO: 19

366 &lt;211&gt; LENGTH: 31

367 &lt;212&gt; TYPE: PRT

368 &lt;213&gt; ORGANISM: Homo sapiens

370 &lt;220&gt; FEATURE:

371 &lt;221&gt; NAME/KEY: misc\_feature

372 &lt;223&gt; OTHER INFORMATION: Partial sequence of MKK7, showing high score in the local alignment

373 between MKK7 and PAK4

376 &lt;400&gt; SEQUENCE: 19

378 Val Val Leu Lys Ser His Asp Cys Pro Tyr Ile Val Gln Cys Phe Gly

379 1 5 10 15

382 Thr Phe Ile Thr Asn Thr Asp Val Phe Ile Ala Met Glu Leu Met

383 20 25 30

386 &lt;210&gt; SEQ ID NO: 20

387 &lt;211&gt; LENGTH: 31

388 &lt;212&gt; TYPE: PRT



**VERIFICATION SUMMARY**

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